FIG. 1A

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

```
GTCGACCCACGCGGTCCGCACTCAACAATGCCTGCCCCTCTCTGACTGCACGTCCGCCGCCGTCCGCGCCTGCCGCGGCC   79

CAAGCCAAGTCGAGCGGCCGTTGCCCACCGACAGCCCTTGGCCCCGGGACCAGGAGGTGAGCCGCGCG   158

                                                             M   H   S   P     4
CGCACAGCTCCGTGGCGCTCGCGCCCGTGCTGAGGCGCCGCCAGGTGCCCCCGCAGCCCGCCGCCGAG ATG CAC AGC CCG   233

 P   G   L   L   A   L   W   L   C   A   V   L   C   A   S   A   R   G   G   S    24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCA GTG CTG TGC GCT TCG GCG GCG GGG GGC AGC   293

 D   P   Q   P   G   P   G   R   P   A   C   P   C   H   C   Q   E   D    44
GAC CCC CAG CCT GGC CCG GGG CGT CCG GCT CCC TGC CCC TGC CAC TGC CAG GAG GAC   353

 G   I   M   L   S   A   D   C   S   E   L   G   L   S   V   V   P   A   D   L    64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG   413

 D   P   L   T   A   Y   L   D   L   S   M   N   N   L   T   E   L   Q   P   G    84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT   473

 L   F   H   H   L   R   F   L   E   E   L   R   L   S   G   N   H   L   S   H   104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGG AAC CAC CTC TCA CAC   533

 I   P   G   Q   A   F   S   G   L   H   S   L   K   I   L   M   L   Q   S   N   124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC   593
```

FIG.1B

```
Q    L   R   G   I   P   A   E   A   L   W   E   L   P   S   L   Q   S   L   R
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC   144
                                                                                   653

L    D   A   N   L   I   S   L   V   P   E   R   S   F   E   G   L   S   L
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC CTC        164
                                                                                   713

R    H   L   W   L   D   D   N   A   L   T   E   I   P   V   R   A   L   N   N
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC   184
                                                                                   773

L    P   A   L   Q   A   M   T   L   A   L   N   H   I   R   H   I   P   D   Y
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC ATC CCT GAC TAT   204
                                                                                   833

A    F   Q   N   L   T   S   L   V   V   L   H   L   H   N   R   I   Q   H
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT   224
                                                                                   893

V    G   T   H   S   F   E   G   L   H   N   L   E   T   L   D   L   N   Y   N
GTG GGG ACC CAC AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTG GAC CTG AAC TAT AAT   244
                                                                                   953

E    L   Q   E   F   P   L   A   I   R   T   L   G   R   L   Q   E   L   G   F
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC   264
                                                                                   1013

H    N   N   I   K   A   I   P   E   K   A   F   M   G   N   P   L   L   Q
CAT AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC CCT CTC CTG CAG        284
                                                                                   1073

T    I   H   F   Y   D   N   P   I   Q   F   V   G   R   S   A   F   Q   Y   L
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG   304
                                                                                   1133
```

FIG. 1C

```
S  K  L  H  T  L  S  L  N  G  A  T  D  I  Q  E  F  P  D  L    324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC  1193

K  G  T  T  S  L  E  I  L  T  R  A  G  I  R  L  L  P         344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA          1253

P  G  V  C  Q  Q  L  P  R  L  R  I  L  E  L  S  H  N  Q  I    364
CCG GGA GTG TGC CAA CAG CTG CCT AGG CTC CGA ATC CTG GAG TCT CAT AAT CAG ATC       1313

E  E  L  P  S  L  H  R  C  Q  K  L  E  E  I  G  L  R  H  N    384
GAG GAG TTA CCC AGC CTG CAC AGA TGT CAG AAG CTG GAG GAA ATT GGC CTC CAT AAC       1373

R  I  K  E  I  G  A  D  T  F  S  Q  L  G  S  L  Q  A  L  D    404
AGG ATC AAG GAA ATT GGT GCA GAT ACC TTC AGC CAG CTG GGC TCC TTG CAA GCT TTA GAC   1433

L  S  W  N  A  I  R  A  I  H  P  E  A  F  S  T  L  R  S  L    424
CTG AGT TGG AAT GCC ATC CGT GCC ATC CAC CCT GAG GCT TTC TCA ACC CTT CGA TCC TTG   1493

V  K  D  L  T  D  N  Q  L  T  L  P  L  A  G  L  G  G         444
GTT AAG GAC CTG ACT GAC AAC CAG CTG ACC ACA CTG CCC CTG GCT GGG CTG GGA GGC        1553

L  M  H  L  K  L  K  G  N  L  A  L  S  Q  A  F  S  K  D  S    464
CTG ATG CAC CTG AAG CTC AAG GGG AAC TTG GCC CTG TCT CAG GCC TTC TCC AAG GAC AGT   1613

F  P  K  L  R  I  L  E  V  P  Y  A  Y  Q  C  C  A  Y  G  I    484
TTC CCA AAA CTG AGG ATC CTG GAG GTG CCC TAC GCC TAC CAG TGC TGT GCC TAC GGC ATC   1673
```

FIG.1D

```
      C   A   S   F   F   K   T   S   G   Q   W   Q   A   E   D   F   H   P   E   E    504
     TGT GCC AGC TTC TTC AAG ACC TCT GGG CAG TGG CAG GCC GAG GAC TTT CAT CCA GAA GAA  1733

      E   E   A   P   K   R   P   L   G   L   L   A   G   Q   A   E   N   H   Y   D    524
     GAG GAG GCA CCA AAG AGG CCC CTG GGT CTC CTT GCT GGA CAA GCT GAG AAC CAC TAT GAC  1793

      L   D   L   D   E   L   Q   M   G   T   E   D   S   K   P   N   P   S   V   Q    544
     CTA GAC CTG GAT GAG CTC CAG ATG GGG ACA GAG GAC TCA AAG CCA AAC CCC AGT GTC CAG  1853

      C   S   P   V   P   G   P   F   K   P   C   E   H   L   F   E   S   W   G   I    564
     TGC AGC CCT GTT CCA GGC CCC TTC AAG CCC TGC GAG CAC CTC TTT GAG AGC TGG GGC ATC  1913

      R   L   A   V   W   A   I   V   L   S   V   L   C   N   G   L   L   V   L   L    584
     CGC CTT GCT GTG TGG GCC ATC GTG CTC TCC GTA CTC TGT AAC GGG CTG CTG GTG CTG CTG  1973

      T   V   F   A   S   G   P   S   P   L   S   P   V   K   L   V   G   A   M        604
     ACA GTC TTT GCC AGC GGA CCC AGC CCG CTG TCC CCC     AAG CTT GTG GGT GCG ATG      2033

      A   G   A   N   A   L   T   G   I   S   C   G   L   L   A   S   V   D   A   L    624
     GCA GGC GCC AAC GCC CTG ACG GGC ATT TCC TGT GGT CTC CTG GCC TCT GTG GAC GCC TTG  2093

      T   Y   G   Q   F   A   E   Y   G   A   R   W   E   S   G   L   G   C   Q   A    644
     ACC TAT GGT CAG TTC GCT GAG TAT GGA GCC CGC TGG GAG AGC GGT CTG GGC TGC CAG GCT  2153

      T   G   F   L   A   V   L   G   S   E   A   S   V   L   L   T   L   A   A        664
     ACG GGC TTC CTG GCT GTC CTG GGT TCA GAG GCG TCG GTG CTG CTC ACA CTG GCG GCC      2213
```

FIG. 1E

```
V   Q   C   S   I   S   V   T   C   V   R   A   Y   G   K   A   P   S   P   G       684
GTG CAG TGC AGC ATC TCT GTG ACC TGC GTC CGA GCC TAC GGG AAG GCG CCG TCG CCT GGC    2273

S   V   R   A   G   C   L   G   C   L   A   L   A   V   L   A   A   L   P           704
AGC GTC CGC GCA GGC TGC CTG GGA TGC CTG GCG CTG GCC GTG CTG GCC GCA GCA CTG CCG    2333

L   A   S   V   G   E   Y   G   L   C   L   P   L   P   Y   A   P   P   E           724
CTG GCC TCG GTG GGA GAG TAT GGC CTG TGC CTC CCA CTC CCC TAC GCC CCA CCC GAG        2393

G   R   P   A   A   L   G   C   L   F   A   L   C   F                               744
GGC CGG CCG GCC GCC CTG GGC TTC GCT CTG TGC CTG AAC TCG CTC TGC TTC                2453

L   V   A   G   A   Y   I   K   L   Y   L   C   D   L   P   R   G   D   F   E       764
CTG GTG GCC GTG GCC TAC ATC AAG CTC TAC TGT GAC CTG CCA CGG GGT GAC TTT GAG        2513

A   V   D   C   A   M   V   R   H   A   W   L   I   F   A   D   G   L               784
GCC GTG GAC TGC GCC ATG GTG CGC CAC GTG TGG CTC ATC TTT GCA GAT GGC CTC            2573

L   Y   C   P   V   A   F   L   S   F   L   G   L   F   P   V   T                   804
CTC TAC TGC CCC GTG GCC TTC CTC AGC TTT GCC CTC ATG TCC CTC GGC GTC CCT ACC        2633

P   E   A   V   K   S   V   L   L   V   L   P   L   P   A   C   L   N   P           824
CCC GAG GCT GTC AAG TCA GTC CTT GTG CTG CTG CCT CTG GCC TGC CTC AAC CCA            2693

L   L   Y   L   L   F   N   P   H   F   R   D   D   L   R   L   W   P   S           844
CTG CTC TAC CTG CTC TTC AAC CCT CAC TTC CGG GAT GAC CTT CGG CTC TGG CCA AGC        2753
```

FIG. 1F

```
    P   R   S   P   G   P   L   A   Y   A   A   A   G   E   L   E   K   S   C    864
    CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC  2813

    D   S   T   Q   A   L   V   A   F   S   D   V   D   L   I   L   E   A   S   E    884
    GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG  2873

    A   G   Q   P   P   G   L   E   T   Y   G   F   P   S   V   T   L   I   S   R    904
    GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA  2933

    H   Q   P   G   A   T   R   L   E   G   N   H   F   I   E   S   D   G   T   K    924
    CAT CAG CCG GGG GCC ACC AGG CTG GAG AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG      2993

    F   G   N   P   Q   P   P   M   K   G   E   L   L   K   A   E   G   A   T    944
    TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG AAG GCA GAG GGA GCC ACT      3053

    L   A   G   C   G   S   S   V   G   G   A   L   W   P   S   G   S   L   F   A    964
    TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC  3113

    S   H   L   *                                                                    968
    TCT CAC TTG TAA                                                                  3125

    ATATCCCTCTGTTTGTCCTCTCCCCATCCAATGATGGCTGCTTATAAAGAAAGACAACTCCAACTCCATAGCAAGA    3204

    TGGCCAACACCTCTGACTCCATTGTTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGTCTTGTCTTGG    3283

    CCTTCAGCTTCACTTTCACCCTGGGCCTTCTCTGTCCAATCCAATACTTCTGACAGAGGCCTGGGAAATTTGCATAGGA  3362
```

FIG.1G

```
GAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGGAG    3441

GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTGTGACATATAGAATATAAAAATG    3520

TGTTCTGCGGTTCCATTAATCTTGACCTATGCTGNGCCAAAGTGCTTCCTGTTAAATACACTTTGGAAGACATTGAAAA     3599

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC    3637
??
```

FIG. 2A

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10

    ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-

    +LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f+++L+

ftmzb048h1

    67 LTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH   114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08

    ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-

    +L+ L L+ N+L+++p+al+ Lp+L++L+ L L+ N ++ +p++f++L+

ftmzb048h1

    115   SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11

    ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-

    +L++L+L++N Lt++p al+nLp L+ L N+++++p+++fqnL+

ftmzb048h1

    163   SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08

    ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL k<-

    +L +L+L nN++++ +++++L++nLe+LdL++N+L+++p + + L+

ftmzb048h1

    211   SLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFPL-AIRTLG 257

FIG.2B

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
```
*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
  +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
```
ftmzb048h1
258 RLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
```
*->nLeeLdLsnNk.LtslppgalsnLpnLeeLdLsnNnLtslppglfqn Lk<-*
  +L++L+L++ +++++p+ l++ ++Le L L + ++lppg++q L+
```
ftmzb048h1
306 KLHTLSLNGATdIQEFPD--LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
```
*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
  +L+ L+Ls+N+++lp+ l+ +++Lee+ L +N+++++ ++f+ L+
```
ftmzb048h1
353 RLRILELSHNQIEELPS--LHRCQKLEEIGLRHNRIKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
```
*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
  +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp  + +L
```
ftmzb048h1
399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446

FIG. 3A-1

Protein (species)*	Function-lgand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich α2-GP (human)	?-?	Serum
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF-β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin,TGF-β fibronectin	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP 1b	PM (EC)
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC
IpaH7.8 (Shigella flexnen)	?-?	?
IpaH4.5 (Shigella flexnen)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length	Consensus sequence					PIR entry
		5	10	15	20	25	
15	28 (A)	.LE.L.L..C-.LT...C.L..aL...-					A31857
	29 (B)	.L.EL.L.N-.LGD.Ga..L...L.P..					
8	24	.L..L.L.N-.L..-L...LL..--					NBHUA2
8	29	.L..L.L.N-.a.....a.a.....					BVBYN1
4	24	.L.L.a.N-..-......L--.-					S03616
8	24	.L..L.L.N-.I..-a.....--					A40757
10	24	.L..L.L.N-.I..-V...a....--					NBHUC8
11	24	.L..L.L.N-.a.-a.....a...--					S05390
12	24	.L..L.L.N-.L..-.....a...--					A41748
6	24	.L..a.L.N-.I..-.....a...--					A41781
6	24	.L..a.L.N-.a..-.....F..--					A35272
7	24	.L..L.L.N-.L..-LP.GL..L---					NBHUIA
14	24	.L..L.L.N-.L..-LP.LF.L---					-
12	20	.L..L.a.N-.L..-LP-.----L--PP					A33950
6	20	.L..LV..N-.L..-LP-.----L--P.					A35149
8	20	.L..L.a.N-.L..-LP-.----L--P.					S18248
19	24	.L..L.L.N-.L..-......F..--					A29943
19	24	.L..L.L.N-.I..-.....F.L---					A36665
7	24	.L..LNL.N-.I..-a...aF.L---					S28464
30	24	.L..L.L.N-.a..-a...F..a--					A29944
16	23	.L..L.LS.N-.L..-aP.a...-L---					-
8	24	.L.L.LSNN-.a..-a.......L---					A34210

FIG. 3B-1

Protein (species)*	Function-lgand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylate cyclase (Saccharomyces Cerevisiae)	Signal transduction-RAS	PM
T-LR (Tyrpanosoma brucel)	?-?	(cytoplasm)
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	?
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	Nucleus
DRT100 (Arabidopsis thaliana)	Recombination-?	?
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Chloroplast
CCR4 (Saccharomyces cerevisiae)	Transcription-?	Cytoplasm
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	?
p34 ribosome-binding protein(rat)	RM membranes-ribosome	Nucleus
Carboxypeptidase N (human)	Stabilization-catalytic subunit	RM membrane
Intermalin (Listeria monocytogenes)	Invasion-?	(cytoplasm)
InIB (Listeria monocytogenes)	?-?	Plasma
		Cell wall
		?

LRR superfamily

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L.L..N-................	TDHUM4
2	23	.L.L.LS.N-.L......:-....--	TVHUTT
3	23	.L..LaT.N--.LTS......:--T	S06943
3	23	.LR.aNLSQN--.L...S-.-:.--	A40026
11	23	.L..a.L..N-...G.aP--a.SL--	JQ1674
5	25	.L..L.a.T-.a......F-.--	A41343
7	25	.L..LaS.T-....LP..a.a--	A34548
6	25	.a..L.a.NN..a.S-a....--	A40077
20	23	.L..L.L..N-..-a..--a..L--	OYBY
18	23	.L..L.LSGC.a..--a..-a..L--	A36359
3	23	.a.LaDI..N--LP..a.....N--.	DDBYD1
5	26	.L..L.a..C..a..:a...a...--P	A25226
5	24	.L..lNL..N--.L.G.IP.S-a.S.--	A46260
9	26	.L..a.L.C.NaTD.a..-L..L.--	A41529
4	23	.L..L.a..N--LT.-LP.E-a...--	S31286
11	22	.L..L.a..N--.I..-a--ENa..L--.	A38439
4	24	.L..LDL..N-.L..-LP..F..L--.	—
12	24	.L..L.L..N-.L.-LP..aF..L--.	A34901
13	22	NL..L.L..n-QISDI.P---L..L--T	A39930
6	22	.L..L.L..N-.L.DI.--L..L--.	C39930

.L..L.L..N*..a..*a****a***a**.**
              5   10   15 20 25

FIG. 4

>human DNA seq.
```
TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA
TTCCCGGGTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTCCAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCG
AGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGA
CCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGT
CTGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGC
AGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTCACCTAAATTCAATT
```

FIG. 5

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVS
CVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLR
RLRPRAGDSGPLAYAAAGELEKSSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

FIG. 6

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

```
        *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL
          +L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp  + +L
fahr  64   SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

          k<-*

fahr  111 M   111
```

FIG. 7A

```
ftmzb048h10          1   MHSPPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSMNNLTE   80
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ftmzb048h10          81  LQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEG  160
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ftmzb048h10          161 LSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLD  240
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ftmzb048h10          241 LNYNELQEFPLAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLSKLHTLSLNGATDIQE  320
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~NTTHYRES-----WYACRYRS-----GIPGST----  400

ftmzb048h10          321 FPDLKGTTSLEILTLTRAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL  400
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               ----H--ASVE-----RSQGLSLP-----AHPASLAALAASNTTASG-------KLEX---------DTFSQLSSL  480

ftmzb048h10          401 QALDLSWNAIRAIHPEAFSTLRSIVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC  480
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC
Fahr_human               QALDLSWNAIRSIHPEAFSTLHSIVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC  560

ftmzb048h10          481 AYGICASFFKTSGQWQAEDFHPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPGPFKPCEHLFE
Aa_of_aambb001d112       AYGICASFFKTSGQWQAEDFHPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPHPSVQCSPVPGPFKPCEHLFE
fahr_human               PYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYLFE
```

FIG. 7B

```
                                                                                      640
561
ftmzb048h10         SWGIRLAVWAIVLLSVLCNGIVLLLTVFASGPSLSPVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL
Aa_of_aambb001d112  SWGIRLAVWAIVLLSVLCNGIVLLLTVFASGPSLSPVKLVVGAMAGANALSGISCGLLASVDALTYGQFAEYGARWESGL
fahr_human          SWGIRLAVWAIVLLSVLCNGIVLLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGL
                    I                                                   TM II

                                                                                      720
641
ftmzb048h10         GCQATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
Aa_of_aambb001d112  GCQATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
fahr_human          GCRATGFLAVLGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPY
                    TM III                                             TM IV

                                                                                      800
721
ftmzb048h10         APPEGRPAALGFAVALVMMNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
Aa_of_aambb001d112  APPEGRPAALGFAVALVMMNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
fahr_human          APPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
                    TM V                                               TM VI

                                                                                      880
801
ftmzb048h10         FPVTPEAVKSVLLVVLPLPACINPLLYLLFNPHFRDDLRRIWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
Aa_of_aambb001d112  FPVTPEAVKSVLLVVLPLPACINPLLYLLFNPHFRDDLRRIWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
fahr_human          FPVTPEAVKSVLLVVLPLPACINPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
                    TM VII

                                                                                      960
881
ftmzb048h10         EASEAGQPPGLETYGFPSVTLISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGSSVGGALWPSG
Aa_of_aambb001d112  EASEAGQPPGLETYGFPSVTLISRHQPGATRLEGNHFVESDGTKFGNPQPPMKGELLLKAEGATLAGCGSSVGGALWPSG
fahr_human          EASEAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGLSGGGGFQPSG

                                                                                      968
961
ftmzb048h10         SLFASHLN
Aa_of_aambb001d112  SLFASHLN
fahr_human          LAFASHVN
```

FIG.8A

```
G   L   H   N   L   E   T   L   D   L   N   Y   N   K   L   Q   E   F   P   V      20
GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAT TAT AAC AAG CTG CAG GAG TTC CCT GTG    60

A   I   R   T   L   G   R   L   Q   E   L   G   F   H   N   N   I   K   A          40
GCC ATC CGG ACC CTG GGC AGA CTG CAG GAA CTG GGG TTC CAT AAC AAC ATC AAG GCC       120

I   P   E   K   A   F   M   G   N   P   L   L   Q   T   I   H   F   Y   D   N       60
ATC CCA GAA AAG GCC TTC ATG GGG AAC CCT CTG CTA CAG ACG ATA CAC TTT TAT GAT AAC   180

P   I   Q   F   V   G   R   S   A   F   Q   Y   L   P   K   L   H   T   L   S       80
CCA ATC CAG TTT GTG GGA AGA TCG GCA TTC CAG TAC CTG CCT AAA CTC CAC ACA CTA TCT   240

L   N   G   A   M   D   I   Q   E   F   P   D   L   K   G   T   L   E             100
CTG AAT GGT GCC ATG GAC ATC CAG GAG TTT CCA GAT CTC AAA GGC ACC AGC CTG GAG       300

I   L   T   L   T   R   A   G   I   R   L   L   P   S   G   M   C   Q   Q   L      120
ATC CTG ACC CTG ACC CGC GCA GGC ATC CGG CTG CTC CCA TCG GGG ATG TGC CAA CAG CTG   360

P   R   L   R   V   L   E   L   S   H   N   Q   I   E   E   L   P   S   L   H      140
CCC AGG CTC CGA GTC CTG GAA CTG TCT CAC AAT CAA ATT GAG GAG CTG CCC AGC CTG CAC   420

R   C   Q   K   L   E   E   I   G   L   Q   H   N   R   I   W   E   I   G   A      160
AGG TGT CAG AAA TTG GAG GAA ATC GGC CTC CAA CAC AAC CGC ATC TGG GAA ATT GGA GCT   480

D   T   F   S   Q   L   S   S   L   Q   A   L   D   L   S   W   N   A   I   R      180
GAC ACC TTC AGC CAG CTG AGC TCC CTG CAA GCC CTG GAT CTT AGC TGG AAC GCC ATC CGG   540
```

FIG.8B

```
                                                                                          200
S   I   H   P   E   A   F   S   T   L   H   S   L   V   K   L   D   L   T   D
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG GTC AAG CTG GAC CTG ACA GAC        600

                                                                                          220
N   Q   L   T   T   L   P   L   A   G   L   G   L   M   H   L   K   L   K
AAC CAG CTG ACC ACA CTG CCC CTG GCT GGA CTT GGG GGC TTG ATG CAT CTG AAG CTC AAA        660

                                                                                          240
G   N   L   A   L   S   Q   A   F   S   K   D   S   F   P   K   L   R   I   L
GGG AAC CTT GCT CTC TCC CAG GCC TTC TCC AAG GAC AGT TTC CCA AAA CTG AGG ATC CTG        720

                                                                                          260
E   V   P   Y   A   Y   Q   C   C   P   Y   G   M   C   A   S   F   F   K   A
GAG GTG CCT TAT GCC TAC CAG TGC TGT CCC TAT GGG ATG TGT GCC AGC TTC TTC AAG GCC        780

                                                                                          280
S   G   Q   W   E   A   E   D   L   H   L   D   D   E   S   K   R   P
TCT GGG CAG TGG GAG GCT GAA GAC CTT CAC CTT GAT GAT GAG TCT TCA AAA AGG CCC            840

                                                                                          300
L   G   L   L   A   R   Q   A   E   N   H   Y   D   Q   D   L   E   L   Q
CTG GGC CTC CTT GCC AGA CAA GCA GAG AAC CAC TAT GAC CAG GAC CTG GAG CTC CAG            900

                                                                                          320
L   E   M   E   D   S   K   P   H   P   S   V   Q   C   S   P   T   P   G   P
CTG GAG ATG GAG GAC TCA AAG CCA CAC CCC AGT GTC CAG TGT AGC CCT ACT CCA GGC CCC        960

                                                                                          340
F   K   P   C   E   Y   L   F   E   S   W   G   I   R   L   A   V   W   A   I
TTC AAG CCC TGT GAG TAC CTC TTT GAA AGC TGG GGC ATC CGC CTG GCC GTG TGG GCC ATC       1020

                                                                                          360
V   L   S   V   L   C   N   G   L   V   L   T   V   F   A   G   G   P
GTG TTG CTC TCC GTG CTC TGC AAT GGA CTG GTG CTG ACC GTG TTC GCT GGC GGG CCT           1080
```

FIG. 8C

```
      A   P   L   P   P   V   K   F   V   G   A   I   A   G   A   N   T   L   T          380
  GCC CCC CTG CCC CCG GTC AAG TTT GTG GTA GGT GCG ATT GCA GGC GCC AAC ACC TTG ACT       1140

      G   I   S   C   G   L   L   A   S   V   D   A   L   T   F   G   Q   F   S   E        400
  GGC ATT TCC TGT GGC CTT CTA GCC TCA GTC GAT GCC CTG ACC TTT GGT CAG TTC TCT GAG       1200

      Y   G   A   R   W   E   T   G   L   G   C   R   A   T   G   F   L   A   V   L        420
  TAC GGA GCC CGC TGG GAG ACG GGG CTA GGC TGC CGG GCC ACT GGC TTC CTG GCA GTA CTT       1260

      G   S   E   A   S   V   L   A   V   Q   C   S   V   S   V                           440
  GGG TCG GAG GCA TCG GTG CTG CTC ACT CTG GCC GCA GTG CAG TGC AGC GTC TCC GTC           1320

      S   C   V   R   A   Y   G   K   S   P   S   L   G   S   V   R   A   G   V   L        460
  TCC TGT GTC CGG GCC TAT GGG AAG TCC CCC TCC CTG GGC AGC GTT CGA GCA GGG GTC CTA       1380

      G   C   L   A   L   A   G   L   A   A   A   L   P   A   S   V   G   E   Y            480
  GGC TGC CTG GCA CTG GCA GGG CTG GCC GCC GCA CTG CCC CTG GCC TCA GTG GGA GAA TAC       1440

      G   A   S   P   L   C   L   Y   P   A   Y   P   E   G   Q   P   A   A   L   G        500
  GGG GCC TCC CCA CTC TGC CTG TAC CCC GCG TAC CCT GAG GGT CAG CCA GCA GCC CTG GGC       1500

      F   T   V   A   L   V   M   N   S   F   C   F   L   V   A   G   A   Y                520
  TTC ACC GTG GCC CTG GTG ATG AAC TCC TTC TGT TTC CTG GTC GCC GGT GCC TAC               1560

      I   K   L   Y   C   D   L   P   R   G   D   F   E   A   V   W   D   C   A   M        540
  ATC AAA CTG TAC TGT GAC CTG CCG CGG GGC GAC TTT GAG GCC GTG TGG GAC TGC GCC ATG       1620
```

FIG. 8D

```
V   R   H   V   A   W   L   I   F   A   D   G   L   Y   C   P   V   A   F              560
GTG AGG CAC GTG GCC TGG CTC ATC TTC GCA GAC GGG CTC TAC TGT CCC GTG GCC TTC         1680

L   S   F   A   S   M   L   G   L   F   P   V   T   P   E   A   V   K   S   V          580
CTC AGC TTC GCC TCC ATG CTG GGC CTC TTC CCT GTC ACG CCC GAG GCC GTC AAG TCT GTC     1740

L   L   V   V   L   P   L   P   A   C   L   N   P   L   L   F   N                      600
CTG CTG GTG GTG CTG CCC CTG CCT GCC TGC CTC AAC CCA CTG CTC TTC AAC                 1800

P   H   F   R   D   D   L   R   R   P   R   A   G   D   S   G   P   L                  620
CCC CAC TTC CGG GAT GAC CTT CGG CGG CCC CGC GCA GGG GAC TCA GGG CCC CTA             1860

A   Y   A   A   A   G   E   L   E   S   S   C   D   S   T   Q   A   L   V              640
GCC TAT GCT GCG GCC GGG GAG CTG GAG AGC TCC TGT GAT TCT ACC CAG GCC CTG GTA         1920

A   F   S   D   V   D   L   I   L   E   A   S   E   A   G   R   P   P   G   L          660
GCC TTC TCT GAT GTG GAT CTC ATT CTG GAA GCT TCT GAA GCT GGG CGG CCC CCT GGG CTG     1980

E   T   Y   G   F   P   S   V   T   L   I   S   C   Q   Q   P   G   A   P   R          680
GAG ACC TAT GGC TTC CCC TCA GTG ACC CTC ATC TCC TGT CAG CAG CCA GGG GCC CCC AGG     2040

L   E   G   S   H   C   V   E   P   E   G   N   H   F   G   N   P   Q   P   S          700
CTG GAG GGC AGC CAT TGT GTA GAG CCA GAG GGG AAC CAC TTT GGG AAC CCC CAA CCC TCC     2100

M   D   G   E   L   L   R   A   E   G   S   T   P   A   G   G   L   S                  720
ATG GAT GGA GAA CTG CTG AGG GCA GAG GGA TCT ACG CCA GCA GGT GGC TTG TCA             2160
```

FIG. 8E

```
       G   G   G   F   Q   P   S   G   L   A   F   A   S   H   V   *
                                                                         737
GGG GGT GGC GGC TTT CAG CCC TCT GGC TTG GCC TTT GCT TCA CAC GTG TAA      2211

ATATCCCTCCCCATTCTTCTTCCCCTCTCCTTCCTCTCCCCTCGGTGAATGATGGCTGCTTCTAAAACA   2290

AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGA   2369

CCATCACCAACGGGTGCCTCTTGGCCTGGCCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTCCTTG   2448

TCATGTCTGAAGCTGTGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGGAAGTAAAGACAGTGAAGGGG   2527

TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTTCCCGTGTGACTCATG   2606

GATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTT   2685

TGGAAGAGATTAAAAAAAAAAAAAA   2711
```

FIG. 9

FIG. 10A

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- -

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq
- -
Query: 15088

Scores for sequence family classification (score includes all domains):
Model   Description   Score   E-value N
-------- -----------   -----   ------- ---
LRR   Leucine Rich Repeat   241.4   1.3e-68 16
LRRNT   Leucine rich repeat N-terminal domain   27.2   0.00038 1
7tm_1   7 transmembrane receptor (rhodopsin family)   7.2   0.14   2

Parsed for domains:
Model   Domain seq-f seq-t   hmm-f hmm-t   score E-value
-------- ------- ----- -----   ----- -----   ----- -------
LRRNT   1/1   34   65 ..   1   31 []   27.2 0.00038
LRR   1/16   67   90 ..   1   23 []   12.4   11
LRR   2/16   91   114 ..   1   23 []   24.2   0.0031
LRR   3/16   115   138 ..   1   23 []   19.9   0.062
LRR   4/16   139   162 ..   1   23 []   16.4   0.7
LRR   5/16   163   186 ..   1   23 []   27.5 0.00031
LRR   6/16   187   210 ..   1   23 []   12.1   13
LRR   7/16   211   234 ..   1   23 []   21.6   0.019
LRR   8/16   235   257 ..   1   23 []   18.2   0.2
LRR   9/16   258   281 ..   1   23 []   19.0   0.11
LRR   10/16   282   305 ..   1   23 []   10.2   32
LRR   11/16   306   328 ..   1   23 []   5.6 1.5e+02
LRR   12/16   329   352 ..   1   23 []   8.8   52
LRR   13/16   353   374 ..   1   23 []   19.2   0.097
LRR   14/16   375   398 ..   1   23 []   16.9   0.49
LRR   15/16   399   422 ..   1   23 []   23.7   0.0042
LRR   16/16   423   446 ..   1   23 []   16.4   0.66
7tm_1   1/2   635   662 ..   51   79 ..   3.4   2.2
7tm_1   2/2   784   827 .. 207 259 .]   1.1   11

FIG. 10B

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

```
            *->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-*
              aCp++C+C +++  l+ dCs++gL +vP dl
    15088   34   ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD   65
```

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              +LdLs N+Lt+l pglf++L+
    15088   67   LTAYLDLSMNnLTELQPGLFHHLR   90
```

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              LeeL+Ls+N+L+++p +fs+L
    15088   91   FLEELRLSGNhLSHIPGQAFSGLY   114
```

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              +L+ L L+nN+L ++p +++ Lp
    15088   115   SLKILMLQNNqLGGIPAEALWELP   138
```

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              +L++L+L+ N ++ +p+ +f++L+
    15088   139   SLQSLRLDANlISLVPERSFEGLS   162
```

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              +L++L+L++N Lt++p +++nLp
    15088   163   SLRHLWLDDNaLTEIPVRALNNLP   186
```

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              L+  L N+++++p+ +f+nL+
    15088   187   ALQAMTLALNrISHIPDYAFQNLT   210
```

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019

```
            *->nLeeLdLsnN.Ltslppglfsnlp<-*
              +L +L+L+nN++++l ++f++L
    15088   211   SLVVLHLHNNrIQHLGTHSFEGLH   234
```

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2
       ->nLeeLdLsnN.LtslppglfsnLp<-
       nLe+LdL++N+L+++p +++ L
  15088 235   NLETLDLNYNkLQEFPV-AIRTLG   257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
       ->nLeeLdLsnN.LtslppglfsnLp<-
       +L+eL ++nN+++ +p+++f + p
  15088 258   RLQELGFHNNnIKAIPEKAFMGNP   281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32
       ->nLeeLdLsnN.LtslppglfsnLp<-
       L+++++ +N+++ + ++f+ Lp
  15088 282   LLQTIHFYDNpIQFVGRSAFQYLP   305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02
       ->nLeeLdLsnN..LtslppglfsnLp<-
       +L++L+L++ +++++p+ +++ +
  15088 306   KLHTLSLNGAmdIQEFPD--LKGTT   328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
       ->nLeeLdLsnN.LtslppglfsnLp<-
       +Le L L + +++ lp+g +++Lp
  15088 329   SLEILTLTRAgIRLLPSGMCQQLP   352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
       ->nLeeLdLsnN.LtslppglfsnLp<-
       +L++L Ls+N++++lp+ ++ ++
  15088 353   RLRVLELSHNqIEELPS--LHRCQ   374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
       ->nLeeLdLsnN.LtslppglfsnLp<-
       +Lee+ L++N++ ++ ++fs+L+
  15088 375   KLEEIGLQHNrIWEIGADTFSQLS   398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
       ->nLeeLdLsnN.LtslppglfsnLp<-
       +L+ LdLs N ++s++p++fs L
  15088 399   SLQALDLSWNaIRSIHPEAFSTLH   422

FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
        +L +LdL +N+Lt+lp  + +L
15088  423   SLVKLDLTDNqLTTLPLAGLGGLM   446
```

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

```
        *->dWpfGsalCklvtaldvvnmyaSillLta<-*
        +W  G ++C+ +++l v+ + aS+llLt+
15088  635   RWETG-LGCRATGFLAVLGSEASVLLLTL   662
```

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

```
        *->lCWlPyfivllldtlc.lsiimsstCelervlptallvtlwLayvNs
        l+  P + + +  +l ++         ++++++++v l++ + +
15088  784   LLYCPVAFLSFASMLGlFPV----------
TPEAVKSVLLVVLPLPA 820
```

```
        clNPilY<-*
        clNP++Y
15088   821 CLNPLLY   827
```

FIG. 11A

Searching for complete domains in SMART

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

- -

HMM file: /ddm/robison/smart/smart/smart.all.hmms

Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

- -

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----------	-----	-------	-
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrnt1		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	------	-----	-----	-----	-----	-----	-------
lrrnt1	1/1	34	70 ..	1	38 []	25.7	0.0011
LRR_PS_2	1/13	64	87 ..	1	24 []	1.9	1.2e+02
LRR_typ_2	1/14	64	88 ..	1	24 []	12.6	2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	20	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	209	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	0.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

LRR_typ_2	10/14	327	350 ..	1	24 []	3.1	29
LRR_bac_2	6/7	351	370 ..	1	20 []	14.6	1.3
LRR_PS_2	10/13	351	372 ..	1	24 []	10.8	8
LRR_sd22_2	3/5	351	372 ..	1	22 []	7.6	16
LRR_typ_2	11/14	351	373 ..	1	24 []	18.8	0.13
LRR_RI_2	4/4	351	378 ..	1	28 []	2.6	19
LRR_PS_2	11/13	373	396 ..	1	24 []	2.3	1e+02
LRR_typ_2	12/14	374	396 ..	1	24 []	6.8	10
LRR_sd22_2	4/5	397	418 ..	1	22 []	7.0	19
LRR_PS_2	12/13	397	419 ..	1	24 []	13.6	3.4
LRR_typ_2	13/14	397	420 ..	1	24 []	30.4	4.3e-05
LRR_bac_2	7/7	421	440 ..	1	20 []	5.8	18
LRR_sd22_2	5/5	421	441 ..	1	22 []	3.7	49
LRR_PS_2	13/13	421	442 ..	1	24 []	5.5	39
LRR_typ_2	14/14	421	444 ..	1	24 []	21.6	0.018

Alignments of top-scoring domains:

lrrntl: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011

```
          *->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-*
             +CPapC+C ++    ++ dCs++gL   +vP dl + t +
  15088   34   ACPAPCHCQEDGIMLSADCSELGLS--AVPGDLDPLTAY   70
```

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02

```
          *->LtsL.qvLdLsnNnLsGeIPsslgn<-*
             L L+ +LdLs NnL+ e+ + l+
  15088   64   LDPLtAYLDLSMNNLT-ELQPGLFH   87
```

FIG. 11D

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
```
                    *->LpnL.reLdLsnNqLtsLPpgaFgg<-*
                       L  L+ LdLs N+Lt+L pg+F++
      15088     64     LDPLtAYLDLSMNNLTELQPGLFHH    88
```

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
```
                    *->PpsLkeLnvsnNrLteLPeL<-*
                       +L+eL+ s+N+L+ P
      15088     89     LRFLEELRLSGNHLSHIPGQ     108
```

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
```
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                       L+ L++L+Ls+N+Ls +IP + ++
      15088     89     LRFLEELRLSGNHLS-HIPGQAFS    111
```

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
```
                    *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                       L+ L+eL+Ls+N+L++P +aF+g
      15088     89     LRFLEELRLSGNHLSHIPGQAFSG    112
```

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
```
                    *->npsLreLdLsnNkl.gdeGaraLaeaLks<-*
                       ++ L+eL+Ls+N+l+++ G  +  ++L s
      15088     89     LRFLEELRLSGNHLsHIPG--QAFSGLYS    115
```

FIG. 11E

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
```
                  *->PpslkeLnvsnNrLteLPeL<-*
                     sLk+L  +nN+L    P+
      15088    113   LYSLKILMLQNNQLGGIPAE      132
```

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
```
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L sL++L L+nN+L G    + l+
      15088    113   LYSLKILMLQNNQLGGIPAEALWE      136
```

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
```
                  *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                     L +L+ L L+nNqL  +P++a++
      15088    113   LYSLKILMLQNNQLGGIPAEALWE      136
```

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
```
                  *->PpslkeLnvsnNrLteLPeL<-*
                     psL++L+ + N ++  Pe
      15088    137   LPSLQSLRLDANLISLVPER      156
```

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
```
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L+sLq+L+L  N +s  +P+ +
      15088    137   LPSLQSLRLDANLIS-LVPERSFE      159
```

FIG. 11F

```
LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
                     *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                        Lp+L++L+L+ N ++ +P++ F+g
        15088    137    LPSLQSLRLDANLISLVPERSFEG       160


LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
                     *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                        L+sL++L L +N L+ eIP     n
        15088    161    LSSLRHlWLDDNALT-EIPVRALN        183


LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
                     *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                        L++Lr+L L++N+Lt++P +a+++
        15088    161    LSSLRHlWLDDNALTEIPVRALNN        184


LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
                     *->LtnLeeLdLsqNkI.....kkiENLde<-*
                        L+ L++L+L +N +++ + + + NL
        15088    161    LSSLRHlWLDDNALteipvRALNNLPA     187


LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
                     *->npsLreLdLsnNklgdeGaraL..aeaLks<-*
                        ++sLr L+L +N l++ +raL++ aL++
        15088    161    LSSLRHlWLDDNALTEIPVRALnnLPALQA  190
```

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25

```
                    *->LtsLqvLdLsnNnLsGeIPssIgn<-*
                       L+ Lq   L+ N++s +IP+  ++
     15088    185    LPALQAMTLALNRIS-HIPDYAFQ    207
```

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062

```
                    *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                       Lp+L+  L  N+++++P+ aFq+
     15088    185    LPALQAMTLALNRISHIPDYAFQN    208
```

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79

```
                    *->LtsLqvLdLsnNnLsGeIPssIgn<-*
                       LtsL+vL+L+nN++           s+
     15088    209    LTSLVVLHLHNNRIQHLGTHSFEG    232
```

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002

```
                    *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                       L++L +L+L+nN+++L    F+g
     15088    209    LTSLVVLHLHNNRIQHLGTHSFEG    232
```

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31

```
                    *->npsLreLdLsnNkLgdeGaraLaeaLks<-*
                       ++sL +L+L nN +   G   + e+L+
     15088    209    LTSLVVLHLHNNRIQHLGTHSF-EGLHN    235
```

FIG. 11H

```
LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
              *->LtnLeeLdLsqNkI.....kkiENLde<-*
                 Lt L++L L +N+I++ +++++E+L++
      15088  209  LTSLVVLHLHNNRIqhlgthSFEGLHN      235


LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
             *->PpsLkeLnvsnNrLteLPeL<-*
                ++L++L+ ++N+L e+P
      15088  233  LHNLETLDLNYNKLQEFPVA       252


LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
             *->LpnLreLdLsnnNqLtsLPpgaFqg<-*
                L+nL++LdL++N+L++ P + +
      15088  233  LHNLETLDLNYNKLQEFPVAI-RT       255


LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
            *->LtsLqvLdLsnNnLsGeIPssLgn<-*
               L++L++LdL++N+L e+P +
      15088  233  LHNLETLDLNYNKLQ-EFPVAIRT       255


LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
             *->PpsLkeLnvsnNrLteLPeL<-*
                +L+eL+ nN+++ Pe
      15088  256  LGRLQELGFHNNNIKAIPEK      275
```

FIG. 11I

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85

```
           *->LtsLqvLdLsnNnLsGeIPssIgn<-*
              L +Lq+L ++nNn+   IP+  +
15088   256   LGRLQELGFHNNNIK-AIPEKAFM      278
```

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026

```
           *->LpnLreLdLsnNqLtsLPpgaFgg<-*
              L+ L+eL  +nN+++++P+ aF g
15088   256   LGRLQELGFHNNNIKAIPEKAFMG      279
```

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29

```
           *->LpnLreLdLsnNqLtsLPpgaFgg<-*
              ++L+ L L + ++ LP+g++q
15088   327   TTSLEILTLTRAGIRLLPSGMCQQ      350
```

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3

```
           *->PpsLkeLnvsnNrLteLPeL<-*
              p+L+ L  s+N+++eLP L
15088   351   LPRLRVLELSHNQIEELPSL       370
```

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8

```
           *->LtsLqvLdLsnNnLsGeIPssIgn<-*
              L++L+vL+Ls+N++  e+Ps l +
15088   351   LPRLRVLELSHNQIE-ELPS-LHR      372
```

FIG. 11J

```
LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
                    *->LtnLeeLdLsqNkiKkiENLde<-*
                       L +L++L+Ls+N+I+ + L+
          15088  351  LPRLRVLELSHNQIEELPSLHR    372


LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
                    *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                       Lp Lr+L Ls+Nq+++LP + ++
          15088  351  LPRLRVLELSHNQIEELP-SLHRC     373


LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
                    *->npsLreLdLsnNklgdeGaraLaeaLks<-*
                       +p+Lr+L Ls+N + + + ++ L++
          15088  351  LPRLRVLELSHNQIEELPSLHRCQKLEE     378


LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
                    *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                       +++L+++ L++N++   +++++
          15088  373  CQKLEEIGLQHNRIWEIGADTFSQ     396


LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
                    *->LpnLreLdLsnNqLtsLPpgaFgg<-*
                       +L+e L++N++ ++ +++F+
          15088  374  -QKLEEIGLQHNRIWEIGADTFSQ     396
```

FIG. 11K

LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19

```
                  *->LtnLeeLdLsqNkIkkiENLde<-*
                     L+ L+ LdLs+N I++i
        15088   397  LSSLQALDLSWNAIRSIHPEAF    418
```

LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4

```
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L+sLq LdLs+N + +I ++ ++
        15088   397  LSSLQALDLSWNAIR-SIHPEAFS    419
```

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05

```
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                     L++L+ LdLs+N+++s++p+aF+
        15088   397  LSSLQALDLSWNAIRSIHPEAFST    420
```

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18

```
                  *->PpsLkeLnvsnNrLteLPeL<-*
                     +sL +L+ +N+Lt+LP
        15088   421  LHSLVKLDLTDNQLTTLPLA    440
```

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49

```
                  *->LtnLeeLdLsqNkIkkiENLde<-*
                     L+ L+ LdL +N+++ + L +
        15088   421  LHSLVKLDLTDNQLTTL-PLAG    441
```

FIG. 11L

LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39

```
              *->LtsLqvldlsnNnLsGeIPsslgn<-*
              L+sL+ LdL +N+L+ ++P    g
  15088  421  LHSLVKLDLTDNQLT-TLPL-AGL          442
```

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018

```
              *->LpnLreldlsnNqLtsLPpgaFqg<-*
              L++L +LdL +NqLt+LP    ++g
  15088  421  LHSLVKLDLTDNQLTTLPLAGLGG          444
```

//

FIG.12A

GAP of: FrGcgManager_101_HTAUB3ha_   check: 2817   from: 1   to: 3637

mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_ITA0FIsO_   check: 3059   from: 1   to: 2711

corrected human LGR6 (analysis o - Import - complete

Symbol comparison table:
/ddm_local/gcg/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

```
            Gap Weight:        12      Average Match:    10.000
         Length Weight:         4      Average Mismatch:  0.000

              Quality:      21826            Length:      3688
                Ratio:      8.051              Gaps:        20
   Percent Similarity:     84.248   Percent Identity:    84.211
```

Match display thresholds for the alignment(s) :

```
            | = IDENTITY
            : = 5
            . = 1
```

FIG. 12B

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_

```
 901 CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT  950
                     |||||||||||||||||||||||||||||| ||| |||
   1 ...............GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT   36

 951 AATGAGCTGCAGGAGTTCCCCTTGGCTATCCGGACCCTGGGCAGACTGCA  1000
     ||  |||||||||||||||  |||| ||||||||||||||||||||||||
  37 AACAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA   86

1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT  1050
     ||| |||| |||||||||||||||||||||| |||||| |= ||||||
  87 GGAACTGGGGGTTCCATAACAACAACATCAAGGCCATCCCCAGAAAAGGCCT  136

1051 TCATGGGCAACCCTCTCCTGCAGACAATACATTTTATGACAACCCAATC  1100
     |||||| ||||| || |||||||| |||| ||| |||||| ||||||||
 137 TCATGGGGAACCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC  186

1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT  1150
     |||||||||||| || |||||||||||||||||| || || ||
 187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT  236
```

FIG. 12C

```
1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCAGACCTCAAAGGCA 1200
     ||| ||||||||| || |||| |||| |||| |||| |||||||
 237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286

1201 CCACTAGCCTGGAGATCCTGACCCCGTGCGGGCATCAGAGACTGCTC 1250
     ||| ||||||||||||||||||| || |||| - ||||| | |||||
 287 CCACCAGCCTGGAGATCCTGACCCCGGCAGGCATCCGGCTGCTC 336

1251 CCACCGGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
     ||| |||| ||||||||||||| |||||||| |||||| |||||
 337 CCATCGGGGATGTGCCAACAGCTGCCCAGCTCCGAGTCCTGGAACTGTC 386

1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
     ||| |||| ||||| |-|||||||||| |||||||||| ||||| |||
 387 TCACAATCAAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG 436

1351 AGGAAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
     |||||| ||||| ||||| |- ||| || = |||||| || || |||
 437 AGGAAATCGGCCTCCAACACAACCGCATCTGGGAAAATTGGAGCTGACACC 486

1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAAATGCCAT 1450
     ||||||||||||| ||||| |||||| | |- |||| |||||| ||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536

1451 CCGTGCCATCCACCCTGAGGCTTTCTCAACCCTTCGATCCTTGGTTAAGC 1500
     ||| ||||||||||||||||||||||| ||| ||| | |||| ||||
 537 CCGGTCCATCCACCCTGAGGCCTTCTCCACCCCCTGCACTCCCCTGGTCAAGC 586
```

FIG. 12D

```
1501  TGGACCTGACTGACAACCAGCTGACCACCACTGCCCCTGGCTGGGCTGGGGA  1550
      ||||||| |||||||| |||||||||||||||||||||| ||  ||
 587  TGGACCTGACAGACAACCAGCTGACCACCACTGCCCCTGGCTGGGACTTGGG  636

1551  GGCCTGATGCACCTGAAGCTCAAAGGGAACTTGGCCCTGTCTCAGGCCCTT  1600
      ||| ||||| |||||||||||||| | || || |||||||
 637  GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCCTT  686

1601  CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTACGCCT  1650
      |||||||||||||||||||||||||||||||||||||| || ||||
 687  CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCT  736

1651  ACCAGTGCTGTGCCTACGGCATCTGTGTGCCCAGCTTCTTCAAGACCTCTGGG  1700
      |||||||| |||| ||||  || ||||| |||||||||||| |||||||
 737  ACCAGTGCTGTGCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG  786

1701  CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGAGGAGGCACCAAAGAG  1750
      |||||| |||| |||| || || | || || || || ||||  ||
 787  CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAG  836

1751  GCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC  1800
      |||||||| |||||| ||||||| || |||||| ||||||||| ||||
 837  GCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC  886

1801  TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCCAGTGTC  1850
      |||||||||||||| ||| || || || |||||||||| ||||||||||
 887  TGGATGAGCTCCAGCTGGGAGATGAGGAGGACTCAAAGCCACACCCCAGTGTC  936
```

FIG. 12E

```
1851  CAGTGCAGCCCTGTTCCAGGCCCCTTCAAGCCCCTGCGAGCACCTCTTTGA  1900
            ||||  |||||   ||  |||||||||||   ||   |||||||||||
 937  CAGTGTAGCCCTACTCCAGGCCCCTTCAAGCCCCTGTGAGTACCTCTTTGA   986

1901  GAGCTGGGGCATCCGCGCCTTGCTGTGTGGGCCATCGTGTCTCTCCGTAC  1950
            ||||||||||| ||  |||||||||| ||  || ||||||||||||||||
 987  AAGCTGGGGCATCCGCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGC  1036

1951  TCTGTAACGGGGCTGGTGCTGCTGACAGTCTTTGCCAGGCGACCCAGCCCCG  2000
            ||||  ||   |||||||||||||||  || |||| ||  ||  |||
1037  TCTGCAATGGACTGGTGCTGCTGACCGTGTTCGCTGGCGGCTGCCCCCC  1086

2001  CTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAACGCCCT  2050
            |||  |||| || |||||  ||  || ||||||||||||||||||| |
1087  CTGCCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAACACCTT  1136

2051  GACGGGCCATTCCTGTGGTCTCCTGGCCTCCTGTGGACGCCTTGACCCTATG  2100
            ||   ||||||| ||   || |||||  || |||  || ||   ||
1137  GACTGGCCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG  1186

2101  GTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTCGGGCTGCCAG  2150
            ||||||| || |||  || |||||||||   || || |||||  |
1187  GTCAGTTCTCTGAGTACGCGGAGCCCGCTGGGAGACGCGGCTAGGCTGCCGG  1236

2151  GCTACGGGCTTCCTGCCTGTGGGTTCAGAGGCGTCGGTGCTGCTGCT  2200
            ||  ||||  |||||||| ||  || ||  ||||||||||||||||||
1237  GCCACTGGCTTCCTGCCAGTACTTGGGTCGGAGGCATCGGTGCTGCTGCT  1286
```

FIG. 12F

```
2201 CACACTGGCGGCCGTGTGCAGTGCAGCATCTCTGTGACCTGGCGTCCGAGCCT 2250
     ||| |||| ||  ||||||||  |||  |||||  ||| |||| |||| ||||
1287 CACTCTGGCGCCGCAGTGCAGCTGCAGCGTCTCCGTGTCCTCCGTGTCCGGGCCT 1336

2251 ACGGGAAGGCGCCGTCGCCTGGCAGCGTCCGGCGCCAGGCGCACTGGGATGC 2300
     | |||||| |  |   |  |||||||  || ||  ||  ||  || || |||
1337 ATGGGAAGTCCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCCTAGGCTGC 1386

2301 CTGGCGCTGGCCGGCCGCCGCAGCACTGGCCTGCGGTGGGAGA 2350
     ||||| ||||| |||  ||||||||| |||||| |||||||||
1387 CTGGCACTGGCAGGGCTGGCCGCCGCCCGGCCCTGGCCTCAGTGGGAGA 1436

2351 GTATGGCGCCCTCCCCACTCTGCCCTACGCCCCACCCGAGGGCCGGC 2400
       || ||||||||||||||||||||||||||| |||| |||| | ||
1437 ATACGGGGCCCTCCCCACTCTGCCCTACGCGCCACCTGAGGGTCAGC 1486

2401 CGGCCGCCCTGGGCTTCGCTGTAGCCCTGGTGATGAATGAACTCGCTCTGC 2450
     | ||| |||||||||| | ||| |||||||||||||| ||||||  |||| 
1487 CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACTCCTTCTGT 1536

2451 TTCCTGGTGGTGGCCGGCGCCTACATCAAGCTCTACTGTGACCTGCCACG 2500
     |||||||| |||||||| |||||||||| || |||||||||||||| |||
1537 TTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCG 1586

2501 GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGCCT 2550
     ||| |||||||||||||||||||||||||||||||||| ||| |||||||
1587 GGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGGAGGCACGTGGCCT 1636
```

FIG. 12G

```
2551 GGCTCATCTTTGCAGATGGCCTCCTCTACTGCCCCGTGGCCTTCCTCAGC 2600
     |||||| |||| |||| |||||||||||||| |||||||||||||||||||
1637 GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGC 1686

2601 TTTGCCTCCATGCTGGGCCTCTTCCCTGTCACCCCCGAGGCTGTCAAGTC 2650
     || |||||||||||||||||||||||||||||| |||||||| ||||||||
1687 TTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGTC 1736

2651 AGTCCTTCTGGTGGTGCTGCCTCTGCCTGCCTCAACCCCACTGCTCT 2700
     ||||||||||||||| |||||||| |||||||||||||||||||||| |
1737 TGTCCTGCTGGTGGTGCTGCCCCCTGCCTGCCTCAACCCCACTGCTGT 1786

2701 ACCTGCTCTTCAACCCTCACTTCCGGGATGACCTTCGGCGGCTCTGGCCA 2750
     |||||||||||||||| ||||||||||||||||||||||||||| ||||
1787 ACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCC 1836

2751 AGCCCTCGGTCCCCCAGGGCCCCTAGCCTACGCTGCCACGGGTGAGCTGGA 2800
     || || | ||||||||||||||||| |||| ||| |||||||||||||
1837 CGGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCCGGGGGGAGCTGGA 1886

2801 GAAGAGCTCCTGCGACTCCACCCAGCGCTGGTGCTTTCTCAGATGTGG 2850
     ||||||||||| || |||| |||||| |||| || |||||| |||||||
1887 GAAGAGCTCCTGTGATTCTACCCAGCCCTGGTAGCCTTCTCTGATGTGG 1936

2851 ATCTTATTCTGGAAGCTTCTGAGGCTTGGGCAGCCTCCTGGGCTAGAGACC 2900
     |||| ||||||||||||||||||| ||| ||| ||| ||||||||||||||
1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCCCCCTGGGCTGGGAGACC 1986
```

FIG. 12H

```
2901 TATGGCTTCCCTTCAGTGACCCTCCATCTCCCGACATCAGCCGGGGGCCAC 2950
     |||||||| ||||||||||||||||||||| || |||| |||| |
1987 TATGGCTTCCCCTCAGTGACCCTCCATCTCCTGCAGCCAGGGGCCCC    2036

2951 CAGGCTGGAGGGAAACCATTTATAGAGTCTGATGGAACCAAGTTTGGGA  3000
     |||||||||| |||| ||||| || || ||| | |||||| |||||||
2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086

3001 ACCCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC  3050
     |||| |||| |||| | |||||||||||||| ||||||| |
2087 ACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGGATCT 2136

3051 ACTTTGGCAGGCTGTGGGCTCTTCCGTGGGTGGAGCCCCTCTGGCCCCTGG 3100
     || | |||| | || | |||||| | | | |||||||
2137 ACGCCAGCAGGTGGAGGCTTGTGTCAGGGGGTGGCGGCTTTCAGCCCCTGG 2186

3101 CTCTCTCTTTGCCTCTCACTTGTAAATATCCCT.............    3133
     || ||||| | ||| || |||||||||||
2187 CTTGGCCTTTGCTTCACACGTGTAAATATCCCCTCCCCATTCTTCTCTTCC 2236

3134 .CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
     |||| || | || ||||| || |||||||||||||| |||
2237 CCTCTCTTCCCTTTCCTCTCCCCGGTGAATGATGGCTGCTTCTAA      2286

3175 AAGAAAGACAACTCCAAC...........TCCATAGCAAGATGGCCAAC 3212
     || ||| ||||| ||| || ||||| ||||| |
2287 AACAAATACAACCAAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAG 2336
```

FIG. 12I

```
3213  ACCTCTGACTCCATTGTT...CCTCTCTCCACGACCCCTAACCAATGAGTG  3259
           || ||||| || |   |||||||    || | |||| | |||
2337  TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG  2385

3260  CTTCCAAGTCTTGCTTTGTCTTGGCCT... TCAGCTTCACTTTCACCCTG  3306
           | || |||| |||||||  ||||||| || ||| |||
2386  CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCCTCAGCTTCACCTTGATACTG  2435

3307  GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT  3353
           |||    || |||  ||  |  || ||||| ||||   ||
2436  GGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT  2485

3354  ...TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC  3400
           ||| | || ||| |||  ||| ||||||||||||     |||
2486  GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG......GGG.  2527

3401  CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGGAGGTCTCACA  3449
           || ||| ||||| |   || ||| |||| | |||||| |||||||||||
2528  ..TG...GAGGGTTGATC.....AGGGCACAGTGGACAGGGAGACCTCACA  2568

3450  GAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTG  3499
           ||||| || ||||||||||  | |         | ||| |||||||
2569  GAGAAAGGC.CTGGAAGGTGATTTCC.......CGTGTGACTC.....  2603

3500  TGACATATAGAATATATAAAAATGTGTTCTGCGTTCCATTAATCTTGACCTAT  3549
            | ||| ||| |||||||||||    ||||| ||||||||||| |||
2604  ..ATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATAT  2651
```

FIG. 12J

```
3550 GCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA   3599
     ||  :|| ||  |||||| |||||||  |||||||||| ||| ||||
2652 GCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATTAAAAA   2701

3600 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGCGGCCGC   3637
     ||||||||||
2702 AAAAAAAAAA..........................   2711
```

FIG. 13A

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nCl_ check: 5092 from: 1 to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match: 2.778
Length Weight:	4	Average Mismatch: -2.248

Quality:	-3424	Length: 968
Ratio:	4.646	Gaps: 0
Percent Similarity: 90.773		Percent Identity: 89.281

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 2
. = 1
```

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nC1_ May 5, 19100 15:04

```
201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
                               ||||||||||||·|||||
  1 ..........................GLHNLETLDLNYNKLQEFP 19

251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
     ||||||||||||||||||||||||||||||||||||||||||||||
 20 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69

301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
     |||| ||| ||||||| ||||||||||||||||||||||||·|·|||
 70 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119

351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
     ||||:|||||||||||||||||||||||||||·|||||||||||| ||
120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169

401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGIMHLKL 450
     |||||||||||| |||||||||||·|||||||||||||||||||||||
170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGIMHLKL 219
```

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
    ||||||||||||||||||||||||||||||||||.||.||||| ||||:|||
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 269

501 HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
    | ::||. |||||| |||||| ||||||:: |||||.||||||| ||
270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 319

551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGIVLLTVFASGPSPLSPVKLIV 600
    |||||.|||||||||||||||||||||||||||||| ||.|| ||| |
320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGIVLLTVFAGGPAPLPPVKFV 369

601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 650
    |||.|||| ||||||||||||||||:||.|||.||||.||.|||||||||
370 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 419

651 LGSEASVLLITLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 700
    |||||||||||||||||.|.|:||||||. || ||||| |||||||||||
420 LGSEASVLLITLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 469

701 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 750
    |||||||||||||||||||||||||||.||||||.|||||||| ||||||
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 519

751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800
    |||||||||||||||||||||||||||||||||||||||||||||||||||
520 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 569

FIG. 13D

```
801 FPVTPEAVKSVLLVVLPLPACINPLLYLLFNPHFRDDLRRLWPSPRSPGP 850
        ||||||||||||||||||||||||||||||||||||   ||     ||
570 FPVTPEAVKSVLLVVLPLPACINPLLYLLFNPHFRDDLRRLRPRAGDSGP 619

851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 900
        |||||||||||||||||||||||||||| |||||||.||||||||||||
620 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 669

901 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 950
        ||| ||| ||||.|.: : ||||| | |||||.|:||.|| .|
670 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 719

951 SVGGALWPSGSLFASHL* 968
        | ||  |||  ||||.|
720 SGGGGFQPSGLAFASHV* 737
```

FIG. 14A

>15088

> Fbh150881 - Import - vector trimmed

CCGCCSGGCGGTGCAGCCCGCCGGGACCGGGAGGCGGCAGCTGCGCGCCACCGCGCCGTGCG
TCCGGGCCCGGCCGCCAGGTGCCCCAGTAGCCCGACCGCGAGATGCCCAGCCCGCCGGGG
GCTCCGGGCGCTATGGCTTTGCGCGCGCTGTGCGCTTCCCGGAGGCCGGGCGGGCGCCCC
CCAGCCCGGCCCGGGGCCCACCGCGCTGCCCCGGCCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGGCTGTCCGCCGGTTCCGGGGACCTGGACCC
CCTGACGGCTTACCTGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGCGCTTCTCTGGAGGAGCTGCGGTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGGTCTTCTACAGCCTGAAATCCTGATGCTGCAGAACAATCAGCT
GGGAGGAATCCCCGAGAGGGGCTGTGTGGAGACGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCCTCCCTCCCGCCA
CCCTCTGGCTGGACGACAATGCACTCACGAGATCCCTGTCAGGGCCCGTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCTGCCCTCAACCGCATCAGCCACATCCCGACTACGCGTT
CCAGAATCTCACCAGCCTTGTGGTGCTGCATTTGCATAACAACCGCATCCAGCATCGGG
GACCCACAGCTTCGAGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCCGTGTGCCATCCGGACCCTGGCAGGAACCCTCTGCTACAGACGAT
CAACAACATCAAGGCCATCCCAGAAAAGGCCTTCATGGGGAAGCCCTGCTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACACTACTCTGAATGGTGCCATGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACCAGCCTGGAGATCCTGACCCTGCGCAGCGCATCGGCTGCTCCCATCGGG
GATGTGCCAACAGCCTGCCCAGGTGTCCGAGTCCTGGAACTGTCTCACAATCAAATTGAGGA
GCTGCCCAGCCTGCCACAGGTGTCACACTTCAGAAATTGGAGGAAATCGGCCCTCCAACAACCGCAT
CTGGGAAATTGGAGGTGTGACACCTTCAGCCAGCTGAGCTCCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACAACCAGCTGACCACCACTGCCCCCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCCAGGCCTTCTCCAAGGACAGTTTCCC

FIG. 14B

```
AAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGTCGTCCCTATGGGATGTGTGC
CAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAAGGCCCCTGGCCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACACCCCAGTGTCCAGTGTAG
CCCTACTCCAGGCCCCCTTCAAGCCCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGGCCT
GGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGGTGCTGCTGACCGT
GTTCGCTGGCGGGCCTGCCCCCCCCCCGTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAACACCTTGACTGGCATTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAGACGGGGCTAGCCTGCCGGGCCACTGG
CTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTCACTCTGGCCGCAGTGCA
GTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCCACTGCCCCCTGGC
CTCAGTGGGAGAATACGGGGCCCTCCCCACTCTGCCCTGCCCTACGCGCCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAACTCCTTCTGTTTCCTGGT
CGTGGCCGGTGCCTACAATCAAACTGTACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGCCCTGGCCTCCATGCTGGCCCCTGTCCTGCCGA
CTGTCCCGGTGGCCTTCCTGCTGTCCTGCTGGTGGTCCCCCTGCTGCCCTGCCCGGGCCCGA
GGCCGGTCAAGTCTGTCTCTTCAACCCCCACTTCGGGATGACCTTCGGCGCGGGCGCAGG
GTACCTGCTCTTCAACCCCCACTTCGGGATGACCTTCGGGCGGGCCGGCAGG
GGACTCAGGGCCCCCAGCCCTAGCCTATGCTGCGCGGGAGCTGGAGAAGAGCTTCGTGATTC
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGATCCTTCATTCTGGAATCTCCTGTGATTC
GCGGCCCCCTGGCCTGAGACCTATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCA
GCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGAACCACTTTGG
GAACCCCCAACCCTCCATGGATGAGAACTGCTCGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTTGGCCTTTGCTTCACA
CGTGTAAAATATCCCCTCCCATTCTTCTTCCCCTTCTCTCCCCTTCCCTCTCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCTATAGC
```

AGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGCCTCTTC
CTTGTCATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAGGCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCATGCATAAAARACTTCCTATTAAAATAAGCT
TTGGRAGAGATT

FIG. 14C

FIG. 15

>15088

MPSPPGLRAIWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNLT
ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKIIMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSF
EGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQHLGTHSFEGLHNLE
TLDLNYNKLQEFPVAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAM
DIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFS
QLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVP
YAYQCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFK
PCEYLFESWGIRLAVWAIVLLSVLCNGIVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEY
GARWETGLGCRATGFLAVLGSEASVLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEY
GASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVA
FLSFASMLGLFPVTPEAVKSVLLVVLPLPACINPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQA
LVAFSDVDLILEASEAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGG
GLSGGGGFQPSGLAFASHV*

FIG. 16A

protein alignment between mouse and human
> LGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778	
Length Weight:	4	Average Mismatch:	-2.248	
Quality:	4495	Length:	968	
Ratio:	4.653	Gaps:	2	
Percent Similarity: 91.097		Percent Identity: 89.855		

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 2
. = 1
```

FrGcgManager_9_PBA0KgkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

FIG. 16B

```
  1  MHSPPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSA   50  Mouse
        |||||  ||| |||| ||||     |||   ||| |||||||||||||||
  1  MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA   50  Human

 51  DCSELGLSVVPADIDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN  100
     |||||||| ||  ||||||||||||||||||||||||||||||||||||||
 51  DCSELGLSAVPGDLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN  100

101  HLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLI  150
     |||||||||||||| ||| ||||:|||||||||||||||||||||||||||
101  HLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLI  150

151  SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRH  200
     |||||||||||||||||||||||||||||||||||||||||||||||| |
151  SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISH  200

201  IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP  250
     |||||||||||||||||||||||||| |||  ||||||| ||||| |||||
201  IPDYAFQNLTSLVVLHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEFP  250

251  LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA  300
      |  |||||||||||||||||||||||||||||||||||||||||||||||
251  VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA  300

301  FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ  350
     |||| ||||||||||| ||||||||||||||||||||||||| .|||
301  FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ  350
```

FIG. 16C

```
351   LPRLRLRIELELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL   400
      ||||||:||||||||||||||||||||||||||.|||| ||
351   LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL   400


401   QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL   450
      |||:||||:| .|||||||.|.|||||||||||||||||||||||||||
401   QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL   450


451   KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF   500
      |||||||||||||||||||||||||||||.||||:|||||| |||:|||
451   KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL   500


501   HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG   550
      | ::|. |||||||  |||||||||||||||||:  ||||.|||||||
501   HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG   550


551   PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV   598
      ||||| |||||||||||||||||||||.|| ||||||||||  |. || ||
551   PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV   600


599   VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV   648
      |||.||.|| |||||||||||||||||.|| ||.|||||||.|.|||||||
601   VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV   650


649   LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA   698
      ||||||||||||||||||||::.:|||||.|| |||||||||||||||||
651   LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA   700
```

FIG. 16D

```
699 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 748
        ||||||||||||||||||||||||.|||| |||||| |||||| ||||||
701 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 750

749 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLIYCPVAFLSFASMLGL 798
        ||||||||||||||||||||||||||||||||||||||||||||||||||
751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLIYCPVAFLSFASMLGL 800

799 FPVTPEAVKSVLIVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 848
        ||||||||||||||||||||||||||||||||||||||| || == |||
801 FPVTPEAVKSVLIVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 850

849 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 898
        |||||||||||||||||||||||||||||||||||| |||||||||||||
851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 900

899 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 948
        ||| |||| ||||.| :| :| |||||||:||:.|.| |||
901 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 950

949 SVGGALWPSGSLFASHL* 966
        | || ||| ||||.|
951 SGGGGFQPSGLAFASHV* 968
```